NCBI Entrez Protein
PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Boo
Search Nucleotide for Go Clear
Limits Preview/Index History Clipboard Details
Display default Show: 1 Send to File Get Subsequence

☐ 1: BAB82497. scavenger recepto...[gi:18146952] BLink, Domains, Links

```
LOCUS       BAB82497                 742 aa            linear   ROD 18-JAN-2002
DEFINITION  scavenger receptor with C-type lectin [Mus musculus].
ACCESSION   BAB82497
VERSION     BAB82497.1  GI:18146952
DBSOURCE    accession AB038519.1
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Nakamura,K., Funakoshi,H., Tokunaga,F. and Nakamura,T.
  TITLE     Molecular cloning of a mouse scavenger receptor with C-type lectin
            (SRCL)(1), a novel member of the scavenger receptor family
  JOURNAL   Biochim. Biophys. Acta 1522 (1), 53-58 (2001)
  MEDLINE   21575692
   PUBMED   11718900
REFERENCE   2  (residues 1 to 742)
  AUTHORS   Nakamura,K. and Nakamura,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medical
            School, Division of Biochemistry, Biomedical Research Center; 2-2
            yamadaoka, Suita, Osaka 565-0871, Japan
            (E-mail:knakamur@onbich.med.osaka-u.ac.jp,
            Tel:81-6-6879-3783(ex.3783), Fax:81-6-6879-3789)
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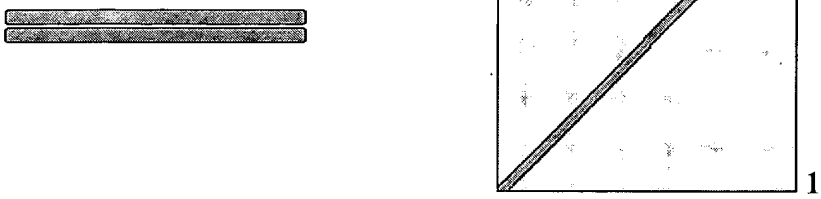
Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 300.0 wordsize: 3 Filter ☐ Align

Sequence 1 gi 17026101 collectin placenta 1 [Homo sapiens] **Length** 742 (1 .. 742)
Sequence 2 gi 18146952 scavenger receptor with C-type lectin [Mus musculus] **Length** 742 (1 .. 742)



NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

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Gapped
Lambda     K      H
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Gap Penalties: Existence: 11, Extension: 1
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Number of extensions: 530
Number of successful extensions: 99
Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
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Number of HSP's gapped (non-prelim): 1
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S1: 42 (21.8 bits)
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S2: 66 (30.0 bits)

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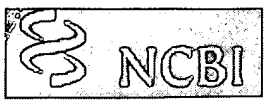

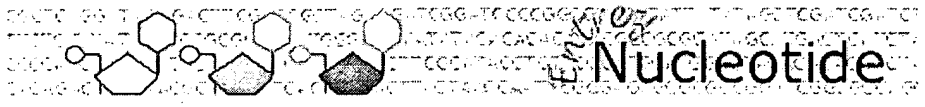

☐ 1: AB005145. Homo sapiens CL-P...[gi:17026100] Links

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VERSION     AB005145.1  GI:17026100
KEYWORDS    .
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  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ohtani,K., Suzuki,Y., Eda,S., Kawai,T., Kase,T., Keshi,H.,
            Sakai,Y., Fukuoh,A., Sakamoto,T., Itabe,H., Suzutani,T.,
            Ogasawara,M., Yoshida,I. and Wakamiya,N.
  TITLE     The membrane-type collectin CL-P1 is a scavenger receptor on
            vascular endothelial cells
  JOURNAL   J. Biol. Chem. 276 (47), 44222-44228 (2001)
  MEDLINE   21570232
   PUBMED   11564734
REFERENCE   2  (bases 1 to 2983)
  AUTHORS   Ohtani,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-1997) Katsuki Ohtani, Asahikawa Medical College,
            Department of Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa,
            Hokkaido 078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp,
            Tel:+81-166-68-2393, Fax:+81-166-68-2399)
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NCBI Entrez Protein
PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Boo
Search Nucleotide for Go Clear
Limits Preview/Index History Clipboard Details
Display default Show: 1 Send to File Get Subsequence

1: BAB39147. scavenger recepto...[gi:13365515] BLink, Domains, Links

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LOCUS       BAB39147                 742 aa            linear   PRI 08-MAR-2001
DEFINITION  scavenger receptor with C-type lectin type I [Homo sapiens].
ACCESSION   BAB39147
VERSION     BAB39147.1  GI:13365515
DBSOURCE    accession AB038518.1
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Nakamura,K., Funakoshi,H., Miyamoto,K., Tokunaga,F. and Nakamura,T.
  TITLE     Molecular cloning and functional characterization of a human
            scavenger receptor with C-type lectin (SRCL), a novel member of a
            scavenger receptor family
  JOURNAL   Biochem. Biophys. Res. Commun. 280 (4), 1028-1035 (2001)
  MEDLINE   21092718
   PUBMED   11162630
REFERENCE   2  (residues 1 to 742)
  AUTHORS   Nakamura,K. and Nakamura,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medical
            School, Division of Biochemistry, Biomedical Research Center; 2-2
            yamadaoka, Suita, Osaka 565-0871, Japan
            (E-mail:knakamur@onbich.med.osaka-u.ac.jp,
            Tel:81-6-6879-3783(ex.3783), Fax:81-6-6879-3789)
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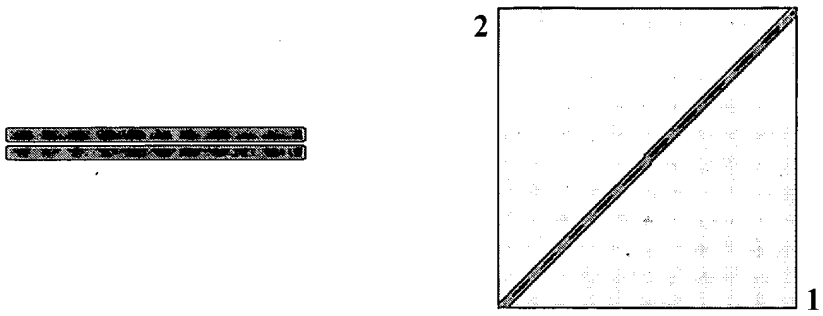
Blast 2 Sequences results

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]

Matrix BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 300.0 wordsize: 3 Filter ☐ Align

Sequence 1	gi 17026101	collectin placenta 1 [Homo sapiens]	**Length** 742 (1 .. 742)
Sequence 2	gi 13365515	scavenger receptor with C-type lectin type I [Homo sapiens]	**Length** 742 (1 .. 742)



NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

```
Score = 1523 bits (3944), Expect = 0.0
Identities = 741/742 (99%), Positives = 741/742 (99%)
```

```
Query: 1   MKDDFAEEEEVQSFGYKRFGIQEGTQCTKCKNNWALKFSIILLYILCALLTITVAILGYK 60
           MKDDFAEEEEVQSFGYKRFGIQEGTQCTKCKNNWALKFSIILLYILCALLTITVAILGYK
Sbjct: 1   MKDDFAEEEEVQSFGYKRFGIQEGTQCTKCKNNWALKFSIILLYILCALLTITVAILGYK 60

Query: 61  VVEKMDNVTGGMETSRQTYDDKLTAVESDLKKLGDQTGKKAISTNSELSTFRSDILDLRQ 120
           VVEKMDNVTGGMETSRQTYDDKLTAVESDLKKLGDQTGKKAISTNSELSTFRSDILDLRQ
Sbjct: 61  VVEKMDNVTGGMETSRQTYDDKLTAVESDLKKLGDQTGKKAISTNSELSTFRSDILDLRQ 120

Query: 121 QLREITEKTSKNKDTLEKLQASGDALVDRQSQLKETLENNSFLITTVNKTLQAYNGYVTN 180
           QLREITEKTSKNKDTLEKLQASGDALVDRQSQLKETLENNSFLITTVNKTLQAYNGYVTN
Sbjct: 121 QLREITEKTSKNKDTLEKLQASGDALVDRQSQLKETLENNSFLITTVNKTLQAYNGYVTN 180

Query: 181 LQQDTSVLQGNLQNQMYSHNVVIMNLNNLNLTQVQQRNLITNLQRSVDDTSQAIQRIKND 240
           LQQDTSVLQGNLQNQMYSHNVVIMNLNNLNLTQVQQRNLITNL@RSVDDTSQAIQRIKND
Sbjct: 181 LQQDTSVLQGNLQNQMYSHNVVIMNLNNLNLTQVQQRNLITNLQRSVDDTSQAIQRIKND 240

Query: 241 FQNLQQVFLQAKKDTDWLKEKVQSLQTLAANNSALAKANNDTLEDMNSQLNSFTGQMENI 300
           FQNLQQVFLQAKKDTDWLKEKVQSLQTLAANNSALAKANNDTLEDMNSQLNSFTGQMENI
Sbjct: 241 FQNLQQVFLQAKKDTDWLKEKVQSLQTLAANNSALAKANNDTLEDMNSQLNSFTGQMENI 300

Query: 301 TTISQANEQNLKDLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHHLRTL 360
           TTISQANEQNLKDLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHHLRTL
Sbjct: 301 TTISQANEQNLKDLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHHLRTL 360
```

```
Query: 361 TSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLRMQQDLMRSRLDTEVANLSVI 420
           TSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLRMQQDLMRSRLDTEVANLSVI
Sbjct: 361 TSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLRMQQDLMRSRLDTEVANLSVI 420

Query: 421 MEEMKLVDSKHGQLIKNFTILQGPPGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGP 480
           MEEMKLVDSKHGQLIKNFTILQGPPGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGP
Sbjct: 421 MEEMKLVDSKHGQLIKNFTILQGPPGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGP 480

Query: 481 AGERGPIGPAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPPGKEGLPGP 540
           AGERGPIGPAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPPGKEGLPGP
Sbjct: 481 AGERGPIGPAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPPGKEGLPGP 540

Query: 541 QGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGPKGPPGPPGPSGAVVPLALQNEPTP 600
           QGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGPKGPPGPPGPSGAVVPLALQNEPTP
Sbjct: 541 QGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGPKGPPGPPGPSGAVVPLALQNEPTP 600

Query: 601 APEDNGCPPHWKNFTDKCYYFSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVG 660
           APEDN CPPHWKNFTDKCYYFSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVG
Sbjct: 601 APEDNSCPPHWKNFTDKCYYFSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVG 660

Query: 661 RESHWIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQWNDF 720
           RESHWIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQWNDF
Sbjct: 661 RESHWIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQWNDF 720

Query: 721 QCEDVNNFICEKDRETVLSSAL 742
           QCEDVNNFICEKDRETVLSSAL
Sbjct: 721 QCEDVNNFICEKDRETVLSSAL 742

CPU time:     0.13 user secs.       0.06 sys. secs          0.19 total secs.

Lambda     K      H
   0.312    0.133    0.393

Gapped
Lambda     K      H
   0.267   0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 19,823
Number of Sequences: 0
Number of extensions: 537
Number of successful extensions: 99
Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 742
length of database: 455,821,981
effective HSP length: 135
effective length of query: 607
effective length of database: 455,821,846
effective search space: 276683860522
effective search space used: 276683860522
T: 9
A: 40
X1: 16 ( 7.2 bits)
X2: 129 (49.7 bits)
```

X3: 129 (49.7 bits)
S1: 42 (21.8 bits)
S2: 66 (30.0 bits)

NiceProt View of Swiss-Prot: P42916

Printer-friendly view | Quick BlastP search

[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

General information about the entry

Entry name	**CL43_BOVIN**
Primary accession number	**P42916**
Secondary accession number	Q8WMF4
Entered in Swiss-Prot in	Release 32, November 1995
Sequence was last modified in	Release 41, February 2003
Annotations were last modified in	Release 42, September 2003

Name and origin of the protein

Protein name	**Collectin-43 [Precursor]**
Synonyms	**CL-43** **43 kDa collectin**
Gene name	**CL43**
From	Bos taurus (Bovine) [TaxID: 9913]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

References

[1] SEQUENCE FROM NUCLEIC ACID.
TISSUE=Liver;
MEDLINE=22414671; PubMed=12527419; [NCBI, ExPASy, EBI, Israel, Japan]
Hansen S., Holm D., Moeller V., Vitved L., Bendixen C., Skjoedt K., Holmskov U.;
"Genomic and molecular characterization of CL-43 and its proximal promoter.";
Biochim. Biophys. Acta 1625:1-10(2003).

[2] SEQUENCE OF 21-321 FROM NUCLEIC ACID, AND PARTIAL SEQUENCE.
TISSUE=Liver;
MEDLINE=94216283; PubMed=8163480; [NCBI, ExPASy, EBI, Israel, Japan]
Lim B.-L., Willis A.C., Reid K.B.M., Lu J., Laursen S.B., Jensenius J.C., Holmskov U.;
"Primary structure of bovine collectin-43 (CL-43). Comparison with conglutinin and lung surfactant protein-D.";
J. Biol. Chem. 269:11820-11824(1994).

Comments

- ***FUNCTION***: LECTIN THAT BINDS TO VARIOUS SUGARS: MANNOSE = MANNAC > FUCOSE > GLCNAC > GLUCOSE = MALTOSE > GALACTOSE > LACTOSE > GALNAC. COULD PLAY A ROLE IN IMMUNE DEFENSE.

- ***SUBUNIT***: OLIGOMERIC COMPLEX OF 4 SET OF HOMOTRIMERS.
- ***SUBCELLULAR LOCATION***: Secreted.
- ***TISSUE SPECIFICITY***: Liver-specific.
- ***PTM***: Hydroxylated *(Potential)*.
- ***SIMILARITY***: Contains 1 collagenous domain.
- ***SIMILARITY***: Contains 1 C-type lectin family domain.

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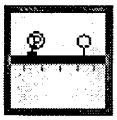
Cross-references

EMBL	AY071821; AAL61855.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	AY071822; AAL61856.1; -.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	X75912; CAA53511.1; ALT_SEQ.	[EMBL / GenBank / DDBJ] [CoDingSequence]
HSSP	P35247; 1B08. [HSSP ENTRY / PDB]	
InterPro	IPR000087; Collagen. IPR001304; Lectin_C. Graphical view of domain structure.	
Pfam	PF00059; lectin_c; 1. PF01391; Collagen; 2.	
SMART	SM00034; CLECT; 1.	
PROSITE	PS00615; C_TYPE_LECTIN_1; 1. PS50041; C_TYPE_LECTIN_2; 1.	
ProDom	[Domain structure / List of seq. sharing at least 1 domain].	
BLOCKS	P42916.	
ProtoNet	P42916.	
ProtoMap	P42916.	
PRESAGE	P42916.	
DIP	P42916.	
ModBase	P42916.	
SWISS-2DPAGE	Get region on 2D PAGE.	

Keywords

Lectin; **Hydroxylation**; **Glycoprotein**; **Mannose-binding**; **Collagen**; **Repeat**; **Calcium**; **Signal**.

Features

 Feature table viewer

Feature aligner

Key	From	To	Length	Description
SIGNAL	1	20	20	
CHAIN	21	321	301	COLLECTIN-43.
DOMAIN	49	162	114	COLLAGEN-LIKE.
DOMAIN	222	321	100	C-TYPE LECTIN (SHORT FORM).
DISULFID	224	319		*BY SIMILARITY*.
DISULFID	297	311		*BY SIMILARITY*.
CONFLICT	125	125		T -> A (IN REF. 2).
CONFLICT	286	286		N -> G (IN REF. 2).

Sequence information

Length: **321 AA** [This is the length of the unprocessed precursor]

Molecular weight: **33615 Da** [This is the MW of the unprocessed precursor]

CRC64: **12BF120BB48861A1** [This is a checksum on the sequence]

```
         10          20          30          40          50          60
          |           |           |           |           |           |
MLPLPLSILL LLTQSQSFLG EEMDVYSEKT LTDPCTLVVC APPADSLRGH DGRDGKEGPQ

         70          80          90         100         110         120
          |           |           |           |           |           |
GEKGDPGPPG MPGPAGREGP SGRQGSMGPP GTPGPKGEPG PEGGVGAPGM PGSPGPAGLK

        130         140         150         160         170         180
          |           |           |           |           |           |
GERGTPGPGG AIGPQGPSGA MGPPGLKGDR GDPGEKGARG ETSVLEVDTL RQRMRNLEGE

        190         200         210         220         230         240
          |           |           |           |           |           |
VQRLQNIVTQ YRKAVLFPDG QAVGEKIFKT AGAVKSYSDA EQLCREAKGQ LASPRSSAEN

        250         260         270         280         290         300
          |           |           |           |           |           |
EAVTQLVRAK NKHAYLSMND ISKEGKFTYP TGGSLDYSNW APGEPNNRAK DEGPENCLEI

        310         320
          |           |
YSDGNWNDIE CREERLVICE F
```

P42916 in FASTA format

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BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

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NiceProt View of Swiss-Prot: Q8MHZ9

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[General] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

Note: most headings are clickable, even if they don't appear as links. They link to the user manual or other documents.

General information about the entry

Entry name	**CL46_BOVIN**
Primary accession number	**Q8MHZ9**
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 41, February 2003
Sequence was last modified in	Release 41, February 2003
Annotations were last modified in	Release 41, February 2003

Name and origin of the protein

Protein name	**Collectin-46 [Precursor]**
Synonyms	**CL-46** **46 kDa collectin**
Gene name	**CL46**
From	Bos taurus (Bovine) [TaxID: 9913]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

References

[1] SEQUENCE FROM NUCLEIC ACID.
Hansen S., Holm D., Moeller V., Vitved L., Bendixen C., Reid K.B.M., Skjoedt K., Holmskov U.;
"CL-46, a novel collectin highly expressed in the bovine thymus and liver.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

Comments

- ***SUBUNIT***: Oligomeric complex of 4 set of homotrimers *(By similarity)*.
- ***SUBCELLULAR LOCATION***: Secreted.
- ***TISSUE SPECIFICITY***: Highly expressed in thymus and liver.
- ***PTM***: Hydroxylated *(Potential)*.
- ***SIMILARITY***: Contains 1 collagenous domain.
- ***SIMILARITY***: Contains 1 C-type lectin family domain.

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Cross-references

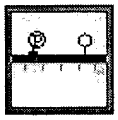
AF509589; AAM34742.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]

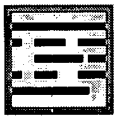
EMBL	AF509590; AAM34743.1; -.[EMBL / GenBank / DDBJ] [CoDingSequence]
InterPro	IPR000087; Collagen. IPR001304; Lectin_C. Graphical view of domain structure.
Pfam	PF00059; lectin_c; 1. PF01391; Collagen; 3.
SMART	SM00034; CLECT; 1.
PROSITE	PS00615; C_TYPE_LECTIN_1; 1. PS50041; C_TYPE_LECTIN_2; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain].
BLOCKS	Q8MHZ9.
ProtoNet	Q8MHZ9.
ProtoMap	Q8MHZ9.
PRESAGE	Q8MHZ9.
DIP	Q8MHZ9.
ModBase	Q8MHZ9.
SWISS-2DPAGE	Get region on 2D PAGE.

Keywords

Lectin; **Hydroxylation**; **Glycoprotein**; **Mannose-binding**; **Membrane**; **Collagen**; **Repeat**; **Calcium**; **Signal**.

Features

 Feature table viewer

 Feature aligner

Key	From	To	Length	Description
SIGNAL	1	20	20	*POTENTIAL.*
CHAIN	21	371	351	COLLECTIN-46.
DOMAIN	46	216	171	COLLAGEN-LIKE.
DOMAIN	273	371	99	C-TYPE LECTIN (SHORT FORM).
SITE	201	203	3	CELL ATTACHMENT SITE (*POTENTIAL*).
DISULFID	275	369		*BY SIMILARITY.*
DISULFID	347	361		*BY SIMILARITY.*
CARBOHYD	90	90		N-LINKED (GLCNAC...) (*POTENTIAL*).

Sequence information

Length: **371 AA** [This is the length of the unprocessed precursor]

Molecular weight: **37445 Da** [This is the MW of the unprocessed precursor]

CRC64: **108AC45A91420E83** [This is a checksum on the sequence]

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MLLLPLSVLL LLTQPWRSLG AEMKIYSQKT LANGCTLVVC RPPEGGLPGR DGQDGREGPQ

        70          80          90         100         110         120
         |           |           |           |           |           |
GEKGDPGSPG PAGRAGRPGP AGPIGPKGDN GSAGEPGPKG DTGPPGPPGM PGPAGREGPS

       130         140         150         160         170         180
         |           |           |           |           |           |
GKQGSMGPPG TPGPKGDTGP KGGMGAPGMQ GSPGPAGLKG ERGAPGELGA PGSAGVAGPA
```

```
       190         200         210         220         230         240
        |           |           |           |           |           |
GAIGPQGPSG ARGPPGLKGD RGDPGERGAK GESGLADVNA LKQRVTILEG QLQRLQNAFS

       250         260         270         280         290         300
        |           |           |           |           |           |
RYKKAVLFPD GQAVGKKIFK TAGAVKSYSD AQQLCREAKG QLASPRSAAE NEAVAQLVRA

       310         320         330         340         350         360
        |           |           |           |           |           |
KNNDAFLSMN DISTEGKFTY PTGESLVYSN WASGEPNNNN AGQPENCVQI YREGKWNDVP

       370
        |
CSEPLLVICE F
```

Q8MHZ9 in FASTA format

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BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

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